

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 29, 2002, 22:06:44 ; Search time 17398.4 Seconds
(without alignments)
1463.857 Million cell updates/sec

Title: US-09-303-518D-463

Perfect score: 1887

Sequence: 1 ttgycattccccaacat.....catatccattatgatag 1887

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

EST:*
1: em_estba:*
2: em_estlum:*
3: em_estlin:*
4: em_estmu:*
5: em_estrov:*
6: em_estcpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	63.8	3.4	997	12	CNS005TE
2	52	2.8	1101	12	CNS0182P
3	50.2	2.7	1101	12	CNS0039G
4	49.6	2.6	1067	12	CNS00C08
5	49.2	2.6	987	12	CNS00A18
6	49	2.6	938	12	CNS006TJ
7	46.4	2.5	1031	12	CNS00CF2
8	46.2	2.4	1101	12	CNS000D1
9	44.6	2.4	1034	12	CNS010B4
10	44.2	2.3	588	12	CNS010B4
11	43.6	2.3	757	12	B21783
12	43.6	2.3	1031	12	CNS03NUU
13	43.4	2.3	797	12	CNS003F8
14	43.2	2.3	1101	12	CNS00F7H
15	43	2.3	1101	12	CNS0039E
16	42.8	2.3	925	12	CNS0091P
17	42.4	2.2	997	12	CNS009XQ

18	42.4	2.2	1101	12	CNS017SY
19	42.2	2.2	467	10	B607950
20	42.2	2.2	572	12	BH233657
21	42.2	2.2	1001	12	CNS0064G
22	41.6	2.2	693	12	AG165805
23	41.6	2.2	943	12	CNS00ZIM
24	41.6	2.2	1101	12	CNS0181N
25	41.4	2.2	1101	12	CNS0106X
26	41.4	2.2	1101	12	CNS017RP
27	41.2	2.2	668	9	AV895698
28	41.1	2.2	1201	12	CNS0163T
29	40.6	2.2	613	10	B607415
30	40.6	2.2	644	10	B607300
31	40.2	2.1	983	12	CNS014HC
32	40.2	2.1	918	12	CNS013Y
33	40	2.1	1080	12	CNS008PP
34	39.8	2.1	512	12	AO866684
35	39.8	2.1	657	10	B6810307
36	39.8	2.1	760	10	BE972622
37	39.8	2.1	1100	12	CNS008EX
38	39.6	2.1	967	12	CNS016XI
39	39.6	2.1	1101	12	CNS006G9
40	39.4	2.1	516	9	AL514527
41	39.4	2.1	651	10	BE846943
42	39.4	2.1	1204	12	CNS016E2
43	39.2	2.1	566	9	AM646687
44	39.2	2.1	681	12	CNS02EDD
45	39.2	2.1	914	12	CNS00C2P
46	39.2	2.1	872	10	B1957771
47	39	2.1	1101	12	CNS00KUZ
48	39	2.1	1201	12	CNS016DO
49	38.8	2.1	971	12	CNS016VO
50	38.8	2.1	1061	12	CNS03LHZ
51	38.8	2.1	1134	12	CNS0307D
52	38.6	2.0	690	12	AG111046
53	38.6	2.0	842	9	BE188368
54	38.6	2.0	947	12	CNS03N8T
55	38.6	2.0	997	12	CNS00K4P
56	38.6	2.0	1101	12	CNS00K4A
57	38.6	2.0	1183	12	CNS016CR
58	38.4	2.0	628	12	B1953999
59	38.4	2.0	859	12	CNS00KIL
60	38.4	2.0	864	12	CNS04NLA
61	38.4	2.0	884	10	B1956488
62	38.4	2.0	1101	12	CNS0006J
63	38.4	2.0	1101	12	CNS017KX
64	38.4	2.0	1157	9	BE036799
65	38.2	2.0	691	12	AG044973
66	38.2	2.0	797	12	AO864430
67	38.2	2.0	1033	10	BE290476
68	38.2	2.0	1101	12	CNS0039L
69	38.2	2.0	1147	12	CNS016ES
70	38.2	2.0	1201	12	CNS0107K
71	38	2.0	1101	12	CNS0007K
72	38	2.0	1101	12	CNS0100X
73	38	2.0	1101	12	CNS016HD
74	38	2.0	1101	12	CNS01768
75	37.8	2.0	463	12	AO815822
76	37.8	2.0	768	12	CNS03EXR
77	37.8	2.0	925	12	CNS002BN
78	37.8	2.0	1101	12	CNS00240
79	37.6	2.0	558	9	AM564214
80	37.6	2.0	644	10	BM164185
81	37.6	2.0	912	12	BH148448
82	37.6	2.0	1101	12	CNS010B3
83	37.6	2.0	1101	12	CNS0182T
84	37.4	2.0	456	12	AO815024
85	37.4	2.0	494	12	AO869337
86	37.4	2.0	625	9	AV924646
87	37.4	2.0	631	12	AG070400
88	37.4	2.0	668	12	AG062735
89	37.4	2.0	826	12	AO912123
90	37.2	2.0	518	10	B1568228

91 37.2 2.0 568 10 BG608064
 92 37.2 2.0 577 9 AL504025
 93 37.2 2.0 585 12 AZ304600
 94 37.2 2.0 759 12 AG056348
 95 37.2 2.0 888 12 AG056348
 96 37.2 2.0 997 12 CENS0204B
 97 37.2 2.0 1002 12 CENS0204B
 98 37.2 2.0 1019 12 CENS0455N
 99 37.2 2.0 1101 12 CENS017KE
 100 37.2 2.0 1627 10 BF792678

ALIGNMENTS

RESULT 1
 LOCUS CENS05TE/c 997 bp DNA linear GSS 03-JUN-1999
 DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
 BACR12K22 of RPCI-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 ACCESSION AL060767.1 GI:4943573
 VERSION AL060767
 KEYWORDS fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 997)
 AUTHORS Direct Submission
 JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 COMMENT Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see <http://www.fruitfly.org> The BDGP Drosophila
 melanogaster BAC library was prepared by Kazutoyo Osoegawa and
 Aaron Mammox in Pieter de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RPCI-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 isogenic strain y2; cn bw sp, the same strain used for the BDGP's
 P1 and EST libraries. A more detailed description of the library
 and how to order individual BAC clones, the entire library, or
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source
 1. 997
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone_lib="RPCI-98"
 /clone="BACR12K22"
 /note="end : TET3"
 BASE COUNT 89 a 99 c 13 g 258 t 538 others
 ORIGIN

Query Match 3.4%; Score 63.8; DB 12; Length 997;
 Best Local Similarity 19.5%; Pred. No. 1.8e-05;
 Matches 98; Conservative 174; Mismatches 231; Indels 0; Gaps 0;

QY 1369 agatggaggggtgttagaagcctaataatgcaactcgtgagcggtggagagaat 1428
 DB 997 AKRARRRGAARARARARARARRRRRGAARARARRRRRRRGAARARARRRRRAG 938
 QY 1429 gttaaggaacgaagaaagagtcagagtcagtttaagccgacgaagaa 1488
 DB 937 AGAARARARARRRRRRRAGRRRAGRRRAGRRRAGRRRAGRRRAGRRRAGRRR 878

QY 1489 tgggaataataacaggttagatttaattcatttagtgytgatatacaataagaa 1548
 DB 877 ARRRARRKARARARARRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 818
 QY 1549 ggaacgttaacagaggaagcctaaaccggtgagtcaggtgagtcagtcacaaacc 1608
 DB 817 ARARARRRRARARARRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 758
 QY 1609 tcggacactgataacatggtgtttcaagcgacgtggaatataaagcctatgga 1668
 DB 757 RARARAGARARARARRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 698
 QY 1669 agttggaggttgaaacgaaggtggaaagtatataccaagacacacattccca 1728
 DB 697 ARRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 638
 QY 1729 aagatgtgagtcaggttagaattgaagtcaggttagtcctggttggaagtagaata 1788
 DB 637 RGARRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 578
 QY 1789 atgcttaagatataatgagcaggtgacaaatgagtcaggttagtataaagattt 1848
 DB 577 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 518
 QY 1849 accgaacctaatagaacagcata 1871
 DB 517 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 495

REFERENCE

AUTHORS
 JOURNAL

COMMENT

RESULT 2
 LOCUS CENS0182P 1101 bp DNA linear GSS 26-JUL-1999
 DEFINITION Drosophila melanogaster genome survey sequence SP6 end of BAC
 BACN37D10 of DrosBAC library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 ACCESSION AL108811.1 GI:5629115
 VERSION AL108811
 KEYWORDS fruit fly.
 SOURCE Drosophila melanogaster
 ORGANISM Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 1101)
 AUTHORS Direct Submission
 JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 COMMENT Determination of this BAC-end sequence was carried out as part of a
 collaboration with the European Drosophila Genome Project (EDGP) -
<http://www.edgp.ebi.ac.uk> - This Drosophila melanogaster BAC
 library (Dros BAC) was made by Alain Billaud at CEPH (Centre
 d'Etude du Polymorphisme Humain) with funding provided by a MRC
 project grant. The DNA was prepared from embryos by Alain Bucheton
 and Genevieve Payan. It has been constructed in the vector
 pBelOBAC11.

FEATURES
 source
 1. 1101
 /organism="Drosophila melanogaster"
 /plasmid="pBelOBAC11"
 /db_xref="taxon:7227"
 /clone_lib="DrosBAC"
 /clone="BACN37D10"
 /note="end : SP6"

BASE COUNT 274 a 268 c 128 g 73 t 358 others
 ORIGIN

Query Match 2.8%; Score 52; DB 12; Length 1101;
 Best Local Similarity 18.5%; Pred. No. 0.022;
 Matches 66; Conservative 152; Mismatches 136; Indels 0; Gaps 0;

QY 1493 aaaaataaacaggttagatttaacatctttagtgggtgatacaataagaagca 1552
Db 706 AAAAAAAGAGGKRRKGGDKGKATKTAAMAKGRKMDGTATWMTWADMTWKA 765
QY 1553 cagtaacagggcagatagctaaccccggtgagtgatgagtgatatacaaacctcg 1612
Db 766 ATDTDAKAAAGRRKRRKRRARRRRARRRRARRRRARRRRARRRRARRRR 825
QY 1613 cactgataaacatcggtggtatcaacgacagctggaataaagcctgagagtt 1672
Db 826 DMDMAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 885
QY 1673 gggagtgagaaagaaagagtcggaagtgatgacacacacacacacacacac 1732
Db 886 RRRARRARRARRARRARRARRARRARRARRARRARRARRARRARRARRARR 945
QY 1733 attgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1792
Db 946 WRDRARRRRARRARRARRARRARRARRARRARRARRARRARRARRARRARR 1005
QY 1793 ttaagataataatgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1848
Db 1006 WMTWRTWMDWMDGRRGRGRRGRGRRGRGRRGRGRRGRGRRGRGRRGRG 1061

RESULT 3
CNS0039G/c 1101 bp DNA linear GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TPT3 end of BAC #
DEFINITION BACR08K10 of RPL-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL063921
VERSION AL063921.1 GI:4941778
KEYWORDS fruit fly.
SOURCE Drosophila melanogaster
ORGANISM Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage;
BP 191 91006 EVRY cedex - FRANCE (E-mail: sequefgenoscope.cns.fr
- Web: www.genoscope.cns.fr)

COMMENT - Web: www.genoscope.cns.fr
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mamoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPL-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center, can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source
1. 1101
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_id="RPL-98"
/clone="BACR08K10"
/note="end: TPT3"
BASE COUNT 201 a 64 c 131 g 202 t 503 others
ORIGIN

Query Match 2.7%; Score 50.2; DB 12; Length 1101;
Best Local Similarity 14.4%; Pred. No. 0.063;

Matches 90; Conservative 269; Mismatches 266; Indels 0; Gaps 0;

QY 1262 gtttcgaatttgagaagcagtgagatatacgaagccgcatatcaagaattat 1321
Db 1090 DRDTRKDDMDWTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMT 1031
QY 1322 cgggagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1381
Db 1030 WMDKMWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMT 971
QY 1382 ataggaagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1441
Db 970 DKDRKDDDDKGGKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRK 911
QY 1442 gaagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1501
Db 910 DDKGKADADDVDTGDDDDKDDKDDKDDKDDKDDKDDKDDKDDKDDK 851
QY 1502 caggttagatttaacatctttagtgggtgagtgagtgagtgagtgagtgag 1561
Db 850 AAADDWADDWADDWADDWADDWADDWADDWADDWADDWADDWADDWADDW 791
QY 1562 gaggcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1621
Db 790 ADDRDAATWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMT 731
QY 1622 aacatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1681
Db 730 TTKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRR 671
QY 1682 aacgaaagaaagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1741
Db 670 WADAATWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMT 611
QY 1742 agcgttagatttgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1801
Db 610 WDRMAADWIDAKADADWIDAKADADWIDAKADADWIDAKADADWIDAKAD 551
QY 1802 ataatgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1861
Db 550 WMAWMAATWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMTWMT 491
QY 1862 gaacagcatatccatitagaata 1886
Db 490 AAAAAAATTTTTTTTTTTTTTAAWTA 466

RESULT 4
CNS00C08 1067 bp DNA linear GSS 04-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TPT3 end of BAC #
DEFINITION BACR24D01 of RPL-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL058564
VERSION AL058564.1 GI:4946142
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1067)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage;
BP 191 91006 EVRY cedex - FRANCE (E-mail: sequefgenoscope.cns.fr
- Web: www.genoscope.cns.fr)

COMMENT - Web: www.genoscope.cns.fr
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and

[illegible]

D6	576	ATTATATGKATGCTGTTCATTAATAAATTAATAATTTTAAANNAANAAN	517
QY	1807	tggcagggtacaagtaacgcggtatcaataagaagattaccgaactaatagaca	1866
D6	516	AAAAAANNANNNANNNANNNANNNANNNANNNANNAAGNANNAANNAANAAAA	457
RESULT	7		
CNS00CF2		CNS00CF2	1031 bp DNA linear GSS 04-JUN-1999
LOCUS		Drosophila melanogaster genome survey sequence TET3 end of BAC #	
DEFINITION		BACR25K05 of RPCL-98 library from Drosophila melanogaster (fruit fly); genomic survey sequence.	
ACCESSION		AL059199	
VERSION		AL059199.1 GI:4946662	
KEYWORDS		GSS.	
SOURCE		Fruit fly.	
ORGANISM		Drosophila melanogaster	
		Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
		Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;	
		Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.	
REFERENCE		1 (bases 1 to 1031)	
AUTHORS		Genoscope.	
TITLE		Direct Submission	
JOURNAL		Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mosmoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCL-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's PI and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.	
FEATURES		Location/Qualifiers	
SOURCE		1..1031	
		/organism="Drosophila melanogaster"	
		/db_xref="taxon:7227"	
		/clone_lib="RPCL-98"	
		/clone="BACR25K05"	
		/note="end : TETP3"	
BASE COUNT		176 a 169 c 124 g 214 t 348 others	
ORIGIN			
Query Match		2.5%; Score 46.4; DB 12; Length 1031;	
Best Local Similarity		20.2%; Pred. No. 0.59;	
Matches		76; Conservative 134; Mismatches 166; Indels 0; Gaps 0;	
QY	1467	taaaagccatcgcaacgaalgygaataaacagggtagatttaacatttat	1526
D6	501	TCAACMMMYCMNTWMAKCATMWMMSNMVYTGAAGCTTDTRTDTDDTTWTWTTTD	560
QY	1527	agtgfgatatalcaataagaagcacgtaaaggaagcagtcgaacccgltgtga	1586
D6	561	TNNTTTKATATWATWITTKRTATTATTCTTTTWWAAATRTDAADKKAAMDTTWGICDADA	620
QY	1587	tgtacgggtatacaacaacacctcgacactgatataacatggggttatacaagcgacagt	1646
D6	621	ATTWMDRTAKTAKTDWDMKWTKTGDTDTWTTWCATPMGARKKRGCKGKKKKKKTRDR	680
QY	1647	ggaataaaaagcctgatggaaggtgggaagtgaaacgaaaaaggtgggaagsgat	1706
D6	661	KGMTTKMKWATRNAGWGATGTAKTDWKATJOTRRRRRGGGGGARGRKADAGRARRK	740

Db 417 TRAGMAAAAAAAAAAAGR-AAAATGAAATATMTAAAAAARAGRWGAAAAAMGTG 359
QY 1502 cagggtagtttaattattttaggtgtagtatacaataaagaagcagtaacag 1501
Db 358 AAAAAAARAGCTAMWMAARRAATGMAAATGCTAAAAATMAARRAAMGAAARAAAA 299
QY 1562 gagggcagtcagtaaccgtgtagtgcagggtagtatacaaacaccgcagctgata 1621
Db 298 WAMRAAAMAAACACCCGAGRAGRAMAAWMTAAACMAGARARAWMTAACMAGAA 239
QY 1622 aacatggggttatacaagcagcagtggaalttaaaagcctgtagaagtggaagtgta 1661
Db 238 AAAGAAARTGARAAAGAAATAGGAAAAAAAMWTRRAAAGAAACCMGACR 179
QY 1682 aacgaaaggggggaagtagtaccagcaccatgttcccaagaattggatg 1741
Db 178 GAARAAATTTMTGATMTGCCAAAAMCCAMARCMRAAMGWTAGRGARWTTGGRAAR 119
QY 1742 agcctagaa 1750
Db 118 WRAAAAAAM 110

RESULT 10
FR0037514/c 588 bp DNA linear GSS 22-OCT-1999
LOCUS FR0037514
DEFINITION Fugu rubripes GSS sequence, clone 054M13a1, genomic survey
sequence.
ACCESSION AL125016
VERSION AL125016.1 GI:6106631
KEYWORDS GSS; genome survey sequence.
SOURCE Takifugu rubripes.
ORGANISM Takifugu rubripes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
1 (bases 1 to 588)
Elgar, G., Clark, M.S., Smith, S., Meek, S., Warner, S., Edwards, Y.J.K.,
Umanita, Y., Williams, G. and Brenner, S.
Direct Submission
Submitted (11-OCT-1999) MRC Human Genome Mapping Project Resource
Centre, Hinxton, Cambridge, CB10 1SB, UK Email:
biohelp@hmp.mrc.ac.uk
Vector: pBluescript II KS
V type: phagemid
PRIMER: KS
DESCR:
One pass dye-terminator sequencing of cosmid cloned genomic
sequence.

FEATURES
Source location/Qualifiers
1..588
/organism="Takifugu rubripes"
/db_xref="taxon:31033"
/clone_id="cosmid 054M13"
/clone="054M13a1"
BASE COUNT 155 a 99 c 112 g 184 t 38 others
ORIGIN

Query Match 2.3%; Score 44.2; DB 12; Length 588;
Best Local Similarity 42.1%; Pred. No. 1.7;
Matches 172; Conservative 0; Mismatches 237; Indels 0; Gaps 0;

QY 1463 agttaaagccatgcgcaagagaaatggaataaacaagggtagatttattcatt 1522
Db 534 AATAAANAACCCGCTCAATCAACCGGTACCTGNCATTTCAATNTAAAGCAATCAGT 475
QY 1523 ttatggtagtgatataaataaagagcagtaacagggggagtagtataacgctg 1582
Db 474 GTCTGTTGGGTTTCTCAANCAATAGTAANCCCAATGANAATTTTGACCTGTGGCTGT 415

QY 1583 gtatgtacgggtgtagatcacacaaccccgacactgataaataatgggttatacagcga 1642
Db 414 GTCTATTTCTNTNACNCTCAAGGCTTCNTGCCCTTAGAGAGACTTATGGCTATTCAGAGA 355
QY 1643 cagtgaaatlaaaagcctgtagaagttggaggtggaacgaataaagtggaag 1702
Db 354 GTCCCTCAAGCCCTTAAACACAGTTTCAANTTGAGAACTGAAGCTTAAATTAACGTTNNT 295
QY 1703 tgatgaccagcaccacatgttcccaagaattggatgtaggctgtaagtgagc 1762
Db 294 TAAGNTTNTNTNACAGCTGCTGTTNTTAATGNTCCCTTAAACTNTAACATTGCTTAAAA 235
QY 1763 ttactcggcttgggaagtagataatgtctaaggaataataatgscaggtacagta 1822
Db 234 TTCTTTTAAGAGCTGATATTAAACGGGTTAAACGGCATATTAAAGTCTAATGACTGATG 175
QY 1823 aatcggtatlaaataagaagattaccgaacctaatagaacagcata 1871
Db 174 ACTGATGTAAATAGACTTAATCTTTACAGTACTTAAATACACAGCA 126

RESULT 11
B21783/c 757 bp DNA linear GSS 16-SEP-1997
LOCUS B21783
DEFINITION F3E7-Sp6 IGF Arabidopsis thaliana genomic clone F3E7, DNA sequence.
ACCESSION B21783
VERSION B21783.1 GI:2396837
KEYWORDS GSS.
SOURCE Thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 757)
Feng, J., Dewar, K., Buehler, E., Kim, C., Li, Y., Shinn, P., Sun, H. and
Ecker, J.
BAC End Sequences at ATGC
Unpublished (1997)
Other GSSs: F3E7-R7
Contact: Ecker, J.
Arabidopsis Thaliana Genome Center
University of Pennsylvania
Dept. of Biology, University of Pennsylvania, Philadelphia, PA
19104
Tel: 215-898-9384
Fax: 215-898-8780
Email: jecker@etgenom.bio.upenn.edu
Seq primer: Sp6
Class: BAC ends
High quality sequence start: 121
High quality sequence stop: 214.

FEATURES
Source location/Qualifiers
1..757
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="F3E7"
/clone_id="IGF"
/sex="thermophilite"
/note="Vector: BelobACII, Site_1: EcoRI, Site_2: EcoRI;
Produced by Thomas Altman"

BASE COUNT 222 a 255 c 73 g 191 t 16 others
ORIGIN

Query Match 2.3%; Score 43.8; DB 12; Length 757;
Best Local Similarity 54.9%; Pred. No. 2.4;
Matches 78; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1407 tcgtgacaggtggagaaatgttcaagaaagagaagaagcagagtagtcaagtt 1466
Db 517 TGTGTTGGTGGGGNCTANAGAAAAAAGAGTGGGNTGTTT 458

Db 402 AAVMTSSVSAVSATSHHWKDTWTKKKAVKMKDKDKKKNNVMMMAADKSKNAK 461

Qy 1617 tgataaacatgggcgtttcaagcgacagctggaaatttaaaagcctgatggaattggga 1676

Db 462 DWKDAAAAAAMMKKKRAKCKDKKSMKKDWVMMATKTAALVNVNAKKKNNNNNNN 521

Qy 1677 ggtgaacacgaaanaaagctgaggaaatgatgacacgaacacacatgtcccaaaatg 1736

Db 522 NKKNNAAATTKAKSMKKDMSBNATBHTDKAKBKHKSCBBAADRDVSVAAAMKGGKG 581

Qy 1737 ggaatgagcctgaatttaagcgtgaagcttaactcgccttgggaagatagaataatgctta 1796

Db 582 KAAVNVKDVBSMAATRWKGRKSVAAAMKDVSSNTBCKDDTTDVKVHDPAMADNVN 641

Qy 1797 ggaataataatgacgaggtacacgaataatcggtataataatagaagattacacgaac 1856

Db 642 AAMVHKAMAVNYAAMMAAAAAMMKMDWMAAAMDMAMMTKBKDDHKRAMCMWRMC 701

Qy 1857 taatagaacagacatacccatlla 1880

Db 702 CCMKMAAAAMTWAAKSCMCATKR 725

RESULT	14
CNS00E7H	
LOCUS	CNS00E7H 1101 bp DNA linear GSS 04-JUN-1998
DEFINITION	Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR3OK03 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION	A1070235
VERSION	A1070235.1 GI:4950277
KEYWORDS	GSS.
SOURCE	fruit fly.

ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
Drosophila melanogaster	1 (bases 1 to 1101)		Genoscope.	
Eukaryota	Genoscope.		Direct Submission	
Eukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	Submitted (02-JUN-1999)		Genoscope - Centre National de Sequençage	
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;				
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.				

JOURNAL
Submitted (02-JUN-1999) Genoscope - Centre National de Séquençage
BP 191 91006 EVRY cedex - FRANCE (E-mail : secret@genoscope.cns.fr)

COMMENT
- Web : www.genoscope.cns.fr
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Oosagawa and
Aatron Mammoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2: cn bw sp, the same strain used for the BDGP's
PI and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BDGP Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES	source	Location/Qualifiers
	1. .1101	
	/organism="Drosophila	melanogaster"
	/db_xref="taxon:7227"	
	/clone_1lp="PBCI-98"	
	/clone="BACR30K03"	
	/note="end : TET3"	
BASE COUNT	359 a 124 c 178 g	174 t 266 others
ORIGIN		

Query Match	2.3%	Score 43.2	DB 12,	Length 1101,
Best Local Similarity	26.4%	Pred. No. 4.1,		
Matches 101; Conservative 109;		Mismatches 170;	Indels 2;	Gaps 1;

QY	1313	aagattatcgtggggggcggtacataccgaagctgaagcgtgtgtttgatatgcgaacccaat	1372
Db	684	MAMAKGTGDKKGGGCGKAMAKAAMKAGARMMNRMAAGCMTTGKAAAMGAKAAGARARRK	743
QY	1373	ggagaggttgatagaagcttaataatgtacaactcgtgagcaggttgagaaaaatgttc	1432
Db	744	AMCADDYAKKGRMMAAATGSAARKKMDKKGMKAKKAKAKAAGAKGARRAMDAMMAG	803
QY	1433	aggaacgagaaagaaggagtcagagtagtcagtttaagcccatgcgcaagagaatggg	1492
Db	804	AKGAAAAAAMAAAMDRKDDGAKMDKGGAAAMAMGAGAKRMGMAGAGRGGAGRGMG	863
QY	1493	aaaaataaacaggttgatttcaatcatcttaagttggtgatatacaataagaagcca	1552
Db	864	AGAAAGARAKAAAYWCGAGGASAAAAARRKRRMAAAGAKAKAKAKARRADDAAYVKKR	923
QY	1553	cagtaacagaaggagcagtagcttaaccgcgttgatgtatcaagggtgatacacaaactcgg	1612
Db	924	KAAAKRRAAAKARGRMAAAGAK--AMMDGRRGAGDAMGNRGAKAKAKRDMAMAGAGDGDG	981
QY	1613	caactgataacaatggggtttatccaagcgcagctggaaattcaaaaaagcctgaatgaagt	1672
Db	982	GAKGARADAKDAGGCGGCGRGARAKAADGCGSARAADAAMAMKAKRGGARMGDAKRGAKAK	1041
QY	1673	ggagaggttgaaaaacgaaaaaagg	1694
Db	1042	DRAGAKDGARRADDGARMAARAGK	1063

RESULT	15		
CNS0039E/C			
LOCUS	CNS0039E	1101 bp	DNA
DEFINITION	Drosophila melanogaster genome survey sequence T7 end of BAC # GSS 03-JUN-1999		

ACCESSION BAR080E10 of Rpci-98 library from *Drosophila melanogaster* (fruit fly), genomic survey sequence.
VERSION AL063919
KEYWORDS AL063919.1 GI:4941776
SOURCE GSS.
ORGANISM fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

REFERENCE AUTHORS TITLE JOURNAL	COMMENT
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 1101) Genoscope.	
Submitted (02-JUN-1999) Direct Submission	
BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr - Web : www.genoscope.cns.fr)	
Determination of this BAC-end sequence was carried out as part of a	

COMMENT

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oseegawa and Aaron Mamosser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RP11-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES	source	Location/Qualifiers
		1. .1101
		/organism="Drosophila melanogaster"
		/db_xref="taxon:7227"
		/clone_1fp="PRCI-98"
		/clone="BACROBE10"
		/note="end : 17"
BASE COUNT	255 a	247 c 92 g 210 t 297 others
ORIGIN		

BASE COUNT	258 a	107 c	60 g	175 t	501 others
ORIGIN	/clone="BACN03K20" /note="end : T7"				

Query Match	2.2%;	Score 41.4;	DB 12;	Length 1101;
Best Local Similarity	17.6%;	Pred. NO. 12;		
Matches	63;	Conservative 149;	Mismatches 145;	Indels 0;
			Gaps	0;

Qy	1507	ttgaatttaaatcatttttagtggtgtgataccaataagaagcagatgaacggggg	1566
Db	657	TKKAAKRDCTADAAKAWDKATKAKAKKAAAKKAAAKATATGDKAKAKAKAAATK	716
Qy	1567	catagtcctaaccgcyggtgtgtatcggtgtatacaacaaccccgcaactgtataaacat	1626
Db	717	RAKRAAWDTWTWTATADAAADAAAGKADKKAKAKAKADADAKRRMWAOKDKRRRAKAKAKA	776
Qy	1627	gggggttatcaagcgacgtggaataataaagccctgtatggaattggaagtgtaaacg	1686
Db	777	ADDAADADAKAKAADAADADDGCGDCKKRRAKDRKKKKKKKDKAMGDKKKAKKDK	836
Qy	1687	aaaaaagctgggaagctgtatgaccaagcacaccatgctcccaagaattggatgaagct	1746
Db	837	AAAAAKDAAGDKAKRRRRAGDKDAKAKAKAKAKAKKDDDDAKATKAKAKAKAKKDK	896
Qy	1747	agaattgagctgaagcttaacttcggtctgggaagtaagataatgcttaagaataataaa	1806
Db	897	AKAKKKKKKKDKDAKAKAKAKADKDDDDDKDKAKADKKKKKKWDKAKKAKDDDD	956
Qy	1807	tgcgaaaggtcaaatgaatcgggtattaaataagaagaattaccggaacctaataga	1863
Db	957	KKDAKAKDKDKDAADAKAWAKAKADADAKAKAKAKAKAAADDDAADAADAKAKAAAKA	1013

RESULT	26
CNS017RP	
LOCUS	
DEFINITION	
	CNS017RP 1101 bp DNA linear GSS 26-JUL-1999
	Drosophila melanogaster genome survey sequence S6 end of BAC
	BACN7J10 of DrosBAC library from Drosophila melanogaster (fruit
	fly) genomic survey sequence.

FEATURES	Location/Qualifiers
source	1. .1101

BASE COUNT	258 a	174 c	277 g	120 t	272 others
ORIGIN					

Query Match	2.28;	Score 41.4;	DB 12,	Length 1101;
Best Local Similarity	25.88;	Pred. No. 12;		
Matches 104;	Conservative 107;	Mismatches 188;	Indels 4;	Gaps 1,

[illegible]

LOCUS	DEFINITION	AV895698	668 bp	mRNA	linear	EST 09-NOV-2000
AV895698	Nori Satoh unpublished cDNA library, young adult Ciona intestinalis cDNA clone rciada2m12 3', mRNA sequence.					

FEATURES	SOURCE
location/Qualifiers	1.668
/organism="Ciona intestinalis"	
/db_xref="taxon:7719"	
/clone="rciad42ml2"	
/clone_lib="Nori Satoh unpublished cDNA library, young adult"	
/tissue_type="whole animal"	
/dev_stage="young adult"	
268 a	97 c 98 g 204 t 1 others
BASE COUNT	
ORIGIN	

Query Match	2.28;	Score 41.2;	DB 9;	Length 666;
Best Local Similarity	48.08;	Pred. No. 11;		

	Matches	118;	Conservative	0;	Mismatches	128;	Indels	0;	Gaps	0;
OY	1536		gatacaacaacttcggccacccgtgataacaatggtgtttatcaagcagacagtggaattaa	1655						
Db	90		GAATAATAGTATACATCAAAACCGTGTAAATATCAATTTTAAATTCGACACGATGTTACCCA	149						
OY	1656		aaagcctgatggaagcttggaagtgaaacgcgaacaaagctggaagaaagtatgaccaagca	1715						
Db	150		ATAATTTGAAATTAATTAATTAGTGTTCGACAGAAATATTGTGAAATAATTAATTAACATATT	209						
OY	1716		caccctgttcccaaaagatggtgataggaagctatgaattgaagctgaagttaacttcggcttg	1775						
Db	210		AGCTAGGTCACCTTGGGTATTTATTAATATAGCTAAGAACTTAAGACCAAAAACACACCGAGAAA	269						
OY	1776		ggaagatgaataatgccttaagaagataataatggaagggtaacaagttaactcggtattaa	1835						
Db	270		AATAAGTACACACATATATATTAATATCAAAAATTTGCAGAAAACAAAACCTTTTAAATG	329						
OY	1836		aataga	1841						
Db	330		AATAAA	335						

RESULT	28		
LOCUS	CNS0163T		
DEFINITION	CNS0163T	1201 bp	DNA
ACCESSION	AL106259		line#r GSS 26-JUL-1999
VERSION	AL106259.1	GI:5620976	
KEYWORDS	GSS.		
SOURCE	fruit fly.		

ORGANISM Drosophila melanogaster
Eukaryota Metazoa: Arthropoda Tracheata Hexapoda Insecta
Pterygota Neoptera Endopterygota Diptera Brachycera
Muscomorpha Ephydroidea Drosophilidae Drosophila
1 (bases 1 to 1201)
Genoscope.
Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Séquençage :
TITLE
REFERENCE
AUTHORS
JOURNAL

COMMENT

Submitted (23-JULY-1999) genoscope - Centre National de séquençage
BP 191 91006 Evry cedex - FRANCE (E-mail : seque@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
<http://www.edgp.ebi.ac.uk/>. This *Drosophila melanogaster* BAC
library (Dros BAC) was made by Alain Billaud at CDPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
Project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBlotBAC11.

FEATURES	SOURCE	Location/Qualifiers
		1. 1201
		/organism="Drosophila melanogaster"
		/plasmid="pBelOBAC11"
		/db_xref="taxon:7227"
		/clone_lib="DrosBAC"
		/clone="BACN15K09"
		/note="end : T7"
BASE COUNT	454 a	123 c 198 g 264 t 162 others
ORIGIN		

Query Match	2.28; Score 41; DB 12; Length 1201;
-------------	-------------------------------------

Matches 114; Conservative 57; Mismatches 179; Indels 0; Gaps 0;

QY 1493 aaataaacaggttagattttaatcatttatagtggtgatatcacaataagaagca 155

Db 805 WAAATTTTWTAAWWAAATTAAATAATTTTWWWWWWTTKKDAAAAATTWMAAAAAAMAAGA 864

QY 1553 caqtaacaqqaqccataqtcctaaccqtcqtaqatatacaqqaqtaatacaacaacacctcqq 161

Db	865	AAATAAAGGGAAAAAATAAATAAATAAAGAAATTCATTCGRRGGACAGAAANNAAGGHWK	924
Oy	1613	caactgataacatgagggttattcaagcgacagtgtgaatitaaagccctgatygaagt	1672
Db	925	GRGRGRRGAAAGCGGAAAAAGRAAARCGGCGRRGGGGAADARRRGAATGGGAAAA	984
Oy	1673	ggagaggtgaaacacgaaanaagctgcgtgaagtgtatgcacagcacaccatggtcccaag	1732
Db	965	RAAATAAAARADAAAAAAGCGRRAAAAAAGRAAGGNAAAAAATAAAAAAAAAAAAAAR	1044
Oy	1733	atctgagatgagcctagaattaaggctcgaagttaactctcggtctgggaagtagaataatgc	1792
Db	1045	RRRGGRAAARRARRRRGGCGRRGRRARANTWAGRRGGGAAAGRRRAAAGGCGAAGRG	1104
Oy	1793	ttaagctaatataatgctcaggtgacagatgaatlcggtgtatataataga	1842
Db	1105	GGAAARAAAAAATAAARARRRRARRAAAAAATAAATAAARAAARAA 1154	

RESULT	29
LOCUS	BG607415
DEFINITION	BG607415 613 bp mRNA linear EST 17-APR-2000 WHE2479.D10.G19ZS Triticum monococcum early reproductive apex cDNA library Triticum monococcum clone WHE2479_D10_G19, mRNA sequence.
ACCESSION	BG607415
VERSION	BG607415.1 GI:13657398
KEYWORDS	EST,
SOURCE	Triticum monococcum.

ORGANISM
Triticum monococcum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poidea;
; Triticeae; Triticum.
1 (bases 1 to 613)
Anderson, O.D., Chao, S., Dubcovsky, J., Echenique, V., Han, P.S., Hsia,
C.C., Kang, Y., Lazo, G.R., Miller, R., Raush, C.J., Seaton, C.L.,
Stamova, B. and Tong, J.C.
The structure and function of the expressed portion of the wheat
genomes - Early reproductive apex cDNA library from Triticum
monococcum

JOURNAL Unpublished (2001)
COMMENT Contact: Olin Anderson

US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: candersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stralagene SK primer.

```
FEATURES      Location/qualifiers
source        1. .613
```

```

/organism="Triticum monococcum"
/cultivar="DV92"
/db_xref="taxon:4568"
/clone="GH2479.D10.G19"
/clone_lib="Triticum monococcum early reproductive apex
cDNA library"
/tissue_type="Early reproductive apex"
/dev_stage="Seven week-old plants"
/lab_host="E. coli XL0LR"
/notes="Vector: Lambda uni-ZAP XR, excised phagemid;
site_1: EcoRI; site_2: XhoI. The tissue, total RNA, and

```

to terminal-spikelet stage during transition from

and the cDNA clones were in vivo excised at the

University of California, Davis (V. Echeverrue, B. Stancov, J. Dubcovsky). Plasmid DNA preparations and DNA

sequencing were performed in the UD Anderson lab (all other authors)."

BASE COUNT	133 a	232 c	148 g	100 t
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Query Match 2.1%; Score 40; DB 12; Length 1080;
 Best Local Similarity 19.4%; Pred. No. 27;
 Matches 90; Conservative 162; Mismatches 211; Indels 0; Gaps 0;

Query Match 2.1%; Score 40; DB 12; Length 1080;
 Best Local Similarity 19.4%; Pred. No. 27;
 Matches 90; Conservative 162; Mismatches 211; Indels 0; Gaps 0;

Query Match 2.1%; Score 39.8; DB 12; Length 512;
 Best Local Similarity 48.9%; Pred. No. 21;
 Matches 107; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

Query Match 2.1%; Score 39.8; DB 12; Length 512;
 Best Local Similarity 48.9%; Pred. No. 21;
 Matches 107; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

Query Match 2.1%; Score 39.8; DB 12; Length 512;
 Best Local Similarity 48.9%; Pred. No. 21;
 Matches 107; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

Query Match 2.1%; Score 39.8; DB 12; Length 512;
 Best Local Similarity 48.9%; Pred. No. 21;
 Matches 107; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

Query Match 2.1%; Score 39.8; DB 12; Length 512;
 Best Local Similarity 48.9%; Pred. No. 21;
 Matches 107; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

Db	992	AMKKKDDKKAKKKAKMKKKDKKKDKKKKKKKKKKKKKKKKKKKKKAAKDAAAAAAANKK	933
OY	1614	accttgtaaacctggggttatcaagcg--acaaigygaaattaaaaagcctgatggagt	1671
Db	932	DKKKDAAKKAANKKKKKKKKKKKKKKKKKKKDAADADAADAAKKAANKKKDKKKDAADKKA	873
OY	1672	tgggaagtgtaaaacgcgaanaaaaggltggyaaaagfatgataccaagaacaccatgftcccaaa	1731
Db	872	AKDAAKKKKKDAKKAADKDAAKKWCKKKKAGGARAANAANKKGCRKGGAGGRRAAA	813
OY	1732	gatttggatgaagccta--gaattaagcctgaagttacttcgccttgygaaagtagaat	1789
Db	812	GATTTTWAATTDTTKTKAGACKTCTTKTKTTTWATTKGAAGKWKTRAAAKDARGDAAATP	753
OY	1790	tgttaagatatataatgycagggcacagtaaatcgggttgtttaaataagaagatt	1849
Db	752	AARAGAATAATKCGGAARAGGAAGACAGAKAKGAANKAGATRGAAATAACMWAAGR	693
OY	1850	cogaactaataagaaca	1866
Db	692	ACWATATGWATRGAAGA	676
RESULT	43		
LOCUS	AM646687/c	566 bp	mRNA linear EST 26-APR-2001
DEFINITION	cm6f03.w1 Blackshear/Soares normalized Xenopus egg library Xenopus laevis cdna clone PBX016F03 5', mRNA sequence.		
ACCESSION	AM646687		
VERSION	AM646687.1	GI:7404183	
KEYWORDS	EST,		
SOURCE	African clawed frog.		
ORGANISM	Xenopus laevis		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amniota; Batrachia; Anura; Mesobatrachia; Pipidea; Piplidae;		
AUTHORS	Xenopodine; Xenopus.		
TITLE	1 (bases 1 to 566)		
JOURNAL	Blackshear,P.J., Lai,W.S., Thorn,J.M., Kennington,E.A., Staffa,N.G.; Ji , Moore,D.T., Boufiard,G.G., Beckstrom-Sternberg,S.M., Touchman ,J.W., Bonaldo,M.F. and Soares,M.B.		
MEDLINE	The NIHES Xenopus maternal EST project: interim analysis of the first 13,879 ESTs from unfertilized eggs		
COMMENT	Gene 267 (1), 71-87 (2001) 21211403 Contact: Perry J. Blackshear Office of Clinical Research and Laboratory of Signal Transduction National Institute of Environmental Health Sciences A2-05 NIEHS, 101 Alexander Drive, Research Triangle Park, NC 27709, USA Tel.: 919 541-4899 Fax: 919 541-4571 Email: black009niehs.nih.gov Clone is available through Research Genetics, Inc., 2130 Memorial Parkway, Huntsville, AL 35901 phone 800-533-4363 ext.cdn, fax 256-536-9016 att:cdn, email cnda@ressgen.com DNA Sequencing and analyses performed by National Institutes of Health Intramural Sequencing Center (NISC). PCR Primers FORWARD: TGTAAACGACGCACACT BACKWARD: CAGGAACAGCTATGCC Plate: 0166 row: F column: 03 Seq primer: T7 primer. Location/Qualifiers 1..566 /organism="Xenopus laevis" /db_xref="taxon:8355" /clone="PBX016F03" /clone_lib="Blackshear/Soares normalized Xenopus egg library" /sex="Female" /tissue_type="unfertilized egg" /cell_type="unfertilized egg"		
FEATURES			
SOURCE			

isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

Source
1. 914
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ORIGIN

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